

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/005,549

DATE: 12/14/2001

TIME: 10:11:22

Input Set : A:\3534107u.app

Output Set: N:\CRF3\12142001\I005549.raw

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3 <110> APPLICANT: BOWEN, MICHAEL A.
 4 WU, YULI
 5 YANG, WEN-PIN
 6 FINGER, JOSHUA
 7 NADLER, STEVEN
 8 CARROLL, PAMELA
 9 FEDER, JOHN
 11 <120> TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING AN ACTIVATED HUMAN
 12 T-LYMPHOCYTE-DERIVED PROTEIN RELATED TO UBIQUITIN
 13 CONJUGATING ENZYME
 15 <130> FILE REFERENCE: D0034np
 C--> 17 <140> CURRENT APPLICATION NUMBER: US/10/005,549
 C--> 18 <141> CURRENT FILING DATE: 2001-10-29
 20 <150> PRIOR APPLICATION NUMBER: 60/308,706
 21 <151> PRIOR FILING DATE: 2001-07-30
 23 <150> PRIOR APPLICATION NUMBER: 60/244,688
 24 <151> PRIOR FILING DATE: 2000-10-30
 26 <160> NUMBER OF SEQ ID NOS: 55
 28 <170> SOFTWARE: PatentIn Ver. 2.1
 30 <210> SEQ ID NO: 1
 31 <211> LENGTH: 2254
 32 <212> TYPE: DNA
 33 <213> ORGANISM: Homo sapiens
 35 <220> FEATURE:
 36 <221> NAME/KEY: CDS
 37 <222> LOCATION: (517)..(1782)
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 44 ccctctccgg ccccgccgg gggcgggcg ccggcggtt tggtagctct agataacctc 180
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 52 ttacccactc ccggaggttg cggcgggcgc atcttggcga aggggggatc aggaagtgcg 420
 54 gaccgcggcg gcgcgggcg cggcgggcgc ggcggagccc ggagcgcagg ccggaggctc 480
 56 ccggccccgc ggccccggag cggagcggag cggagg atg cag cag ccg cag ccg 534
 57 Met Gln Gln Pro Gln Pro
 58 1 5
 60 cag ggg cag cag cag ccg ggg ccg ggg cag cag ctg ggg ggc cag ggg 582
 61 Gln Gly Gln Gln Pro Gly Pro Gly Gln Gln Leu Gly Gly Gln Gly
 62 10 15 20
 64 gcg gcg ccg ggg gcc ggg ggc cca ggg ggg ggc ccg ggg ccg ggg 630
 65 Ala Ala Pro Gly Ala Gly Gly Gly Pro Gly Gly Gly Pro Gly Pro Gly
 66 25 30 35
 68 ccc tgc ctg agg cga gag ctg aag ctg ctc gag tcc atc ttc cac cgc 678
 69 Pro Cys Leu Arg Arg Glu Leu Lys Leu Leu Glu Ser Ile Phe His Arg
 70 40 45 50

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72 ggc cac gag cgc ttc cgc att gcc agc gcc tgc ctg gac gag ctg agc 726
73 Gly His Glu Arg Phe Arg Ile Ala Ser Ala Cys Leu Asp Glu Leu Ser
74 55 60 65 70
76 tgc gag ttc ctg ctg gct ggg gcc gga ggg gcc ggg gcg ggg gcc gcg 774
77 Cys Glu Phe Leu Leu Ala Gly Ala Gly Gly Ala Gly Ala Gly Ala Ala
78 75 80 85
80 ccc gga ccg cat ctc ccc cca cgg ggg tcg gtg cct ggg gat cct gtc 822
81 Pro Gly Pro His Leu Pro Pro Arg Gly Ser Val Pro Gly Asp Pro Val
82 90 95 100
84 cgc atc cac tgc aac atc acg gag tca tac cct gct gtg ccc ccc atc 870
85 Arg Ile His Cys Asn Ile Thr Glu Ser Tyr Pro Ala Val Pro Pro Ile
86 105 110 115
88 tgg tcg gtg gag tct gat gac cct aac ttg gct gct gtc ttg gag agg 918
89 Trp Ser Val Glu Ser Asp Asp Pro Asn Leu Ala Ala Val Leu Glu Arg
90 120 125 130
92 ctg gtg gac ata aag aaa ggg aat act ctg cta ttg cag cat ctg aag 966
93 Leu Val Asp Ile Lys Lys Gly Asn Thr Leu Leu Gln His Leu Lys
94 135 140 145 150
96 agg atc atc tcc gac ctg tgt aaa ctc tat aac ctc cct cag cat cca 1014
97 Arg Ile Ile Ser Asp Leu Cys Lys Leu Tyr Asn Leu Pro Gln His Pro
98 155 160 165
100 gat gtg gag atg ctg gat caa ccc ttg cca gca gag cag tgc aca cag 1062
101 Asp Val Glu Met Leu Asp Gln Pro Leu Pro Ala Glu Gln Cys Thr Gln
102 170 175 180
104 gaa gac gtg tct tca gaa gat gaa gat gag gag atg cct gag gac aca 1110
105 Glu Asp Val Ser Ser Glu Asp Glu Asp Glu Glu Met Pro Glu Asp Thr
106 185 190 195
108 gaa gac tta gat cac tat gaa atg aaa gag gaa gag cca gct gag ggc 1158
109 Glu Asp Leu Asp His Tyr Glu Met Lys Glu Glu Glu Pro Ala Glu Gly
110 200 205 210
112 aag aaa tct gaa gat gat ggc att gga aaa gaa aac ttg gcc atc cta 1206
113 Lys Lys Ser Glu Asp Asp Gly Ile Gly Lys Glu Asn Leu Ala Ile Leu
114 215 220 225 230
116 gag aaa att aaa aag aac cag agg caa gat tac tta aat ggt gca gtg 1254
117 Glu Lys Ile Lys Lys Asn Gln Arg Gln Asp Tyr Leu Asn Gly Ala Val
118 235 240 245
120 tct ggc tcg gtg cag gcc act gac cgg ctg atg aag gag ctc agg gat 1302
121 Ser Gly Ser Val Gln Ala Thr Asp Arg Leu Met Lys Glu Leu Arg Asp
122 250 255 260
124 ata tac cga tca cag agt ttc aaa ggc gga aac tat gca gtc gaa ctc 1350
125 Ile Tyr Arg Ser Gln Ser Phe Lys Gly Gly Asn Tyr Ala Val Glu Leu
126 265 270 275
128 gtg aat gac agt ctg tat gat tgg aat gtc aaa ctc ctc aaa gtt gac 1398
129 Val Asn Asp Ser Leu Tyr Asp Trp Asn Val Lys Leu Leu Lys Val Asp
130 280 285 290
132 cag gac agc gct ttg cac aac gat ctc cag atc ctc aaa gag aaa gaa 1446
133 Gln Asp Ser Ala Leu His Asn Asp Leu Gln Ile Leu Lys Glu Lys Glu
134 295 300 305 310
136 gga gcc gac ttc att cta ctt aac ttt tcc ttt aaa gat aac ttt ccc 1494

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137 Gly Ala Asp Phe Ile Leu Leu Asn Phe Ser Phe Lys Asp Asn Phe Pro
138           315           320           325
140 ttt gac cca cca ttt gtc agg gtt gtg tct cca gtc ctc tct gga ggg 1542
141 Phe Asp Pro Pro Phe Val Arg Val Val Ser Pro Val Leu Ser Gly Gly
142           330           335           340
144 tat gtt ctg ggc gga ggg gcc atc tgc atg gaa ctt ctc acc aaa cag 1590
145 Tyr Val Leu Gly Gly Gly Ala Ile Cys Met Glu Leu Leu Thr Lys Gln
146           345           350           355
148 ggc tgg agc agt gcc tac tcc ata gag tca gtg atc atg cag atc agt 1638
149 Gly Trp Ser Ser Ala Tyr Ser Ile Glu Ser Val Ile Met Gln Ile Ser
150           360           365           370
152 gcc aca ctg gtg aag ggg aaa gca cga gtg cag ttt gga gcc aac aaa 1686
153 Ala Thr Leu Val Lys Gly Lys Ala Arg Val Gln Phe Gly Ala Asn Lys
154 375           380           385           390
156 tct caa tac agt ctg aca aga gca cag cag tcc tac aag tcc ttg gtg 1734
157 Ser Gln Tyr Ser Leu Thr Arg Ala Gln Gln Ser Tyr Lys Ser Leu Val
158           395           400           405
160 cag atc cac gaa aaa aac ggc tgg tac aca ccc cca aaa gaa gac ggc 1782
161 Gln Ile His Glu Lys Asn Gly Trp Tyr Thr Pro Pro Lys Glu Asp Gly
162           410           415           420
164 taaccctgga gtatcaccct tctccctcc ccaggcacca ctggaccaat tacctttgaa 1842
166 tgctgtatatt ggtatctcag ctgcctctgt ggttccctcc ctcatTTTTc ctggacgtga 1902
168 tagctctgcc tattgcagga caatgatggc tattctaaac gctaaggaaa aaaaacaaac 1962
170 acagaactgt ttcaagtact caagactgac ttacagacca accaaccacc ttgctggaac 2022
172 ccttgctagc aggcattctt ataaaagaaa ctttcgagcc tcttatatt gctggaaact 2082
174 cagctgtgct ccagactaga gcctccttac ctatgctatg gatttttaat ttattttctc 2142
176 ttatttcatg tacactgctt tttttgggta cagtgtatga tggatgtgta tgaaaaaaat 2202
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182 <211> LENGTH: 422
183 <212> TYPE: PRT
184 <213> ORGANISM: Homo sapiens
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188 1 5 10 15
190 Gln Leu Gly Gly Gln Gly Ala Ala Pro Gly Ala Gly Gly Gly Pro Gly
191 20 25 30
193 Gly Gly Pro Gly Pro Gly Pro Cys Leu Arg Arg Glu Leu Lys Leu Leu
194 35 40 45
196 Glu Ser Ile Phe His Arg Gly His Glu Arg Phe Arg Ile Ala Ser Ala
197 50 55 60
199 Cys Leu Asp Glu Leu Ser Cys Glu Phe Leu Leu Ala Gly Ala Gly Gly
200 65 70 75 80
202 Ala Gly Ala Gly Ala Ala Pro Gly Pro His Leu Pro Pro Arg Gly Ser
203 85 90 95
205 Val Pro Gly Asp Pro Val Arg Ile His Cys Asn Ile Thr Glu Ser Tyr
206 100 105 110
208 Pro Ala Val Pro Pro Ile Trp Ser Val Glu Ser Asp Asp Pro Asn Leu
209 115 120 125

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211 Ala Ala Val Leu Glu Arg Leu Val Asp Ile Lys Lys Gly Asn Thr Leu
212      130      135      140
214 Leu Leu Gln His Leu Lys Arg Ile Ile Ser Asp Leu Cys Lys Leu Tyr
215 145      150      155      160
217 Asn Leu Pro Gln His Pro Asp Val Glu Met Leu Asp Gln Pro Leu Pro
218      165      170      175
220 Ala Glu Gln Cys Thr Gln Glu Asp Val Ser Ser Glu Asp Glu Asp Glu
221      180      185      190
223 Glu Met Pro Glu Asp Thr Glu Asp Leu Asp His Tyr Glu Met Lys Glu
224      195      200      205
226 Glu Glu Pro Ala Glu Gly Lys Lys Ser Glu Asp Asp Gly Ile Gly Lys
227      210      215      220
229 Glu Asn Leu Ala Ile Leu Glu Lys Ile Lys Lys Asn Gln Arg Gln Asp
230 225      230      235      240
232 Tyr Leu Asn Gly Ala Val Ser Gly Ser Val Gln Ala Thr Asp Arg Leu
233      245      250      255
235 Met Lys Glu Leu Arg Asp Ile Tyr Arg Ser Gln Ser Phe Lys Gly Gly
236      260      265      270
238 Asn Tyr Ala Val Glu Leu Val Asn Asp Ser Leu Tyr Asp Trp Asn Val
239      275      280      285
241 Lys Leu Leu Lys Val Asp Gln Asp Ser Ala Leu His Asn Asp Leu Gln
242      290      295      300
244 Ile Leu Lys Glu Lys Glu Gly Ala Asp Phe Ile Leu Leu Asn Phe Ser
245 305      310      315      320
247 Phe Lys Asp Asn Phe Pro Phe Asp Pro Pro Phe Val Arg Val Val Ser
248      325      330      335
250 Pro Val Leu Ser Gly Gly Tyr Val Leu Gly Gly Gly Ala Ile Cys Met
251      340      345      350
253 Glu Leu Leu Thr Lys Gln Gly Trp Ser Ser Ala Tyr Ser Ile Glu Ser
254      355      360      365
256 Val Ile Met Gln Ile Ser Ala Thr Leu Val Lys Gly Lys Ala Arg Val
257      370      375      380
259 Gln Phe Gly Ala Asn Lys Ser Gln Tyr Ser Leu Thr Arg Ala Gln Gln
260 385      390      395      400
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265 Pro Pro Lys Glu Asp Gly
266      420
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270 <211> LENGTH: 471
271 <212> TYPE: PRT
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279      20      25      30
281 Asp Glu Leu Ser Met Lys Phe Ile Asn Ala Glu Asn Lys Gly Ile Ile
282      35      40      45

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284 Val Thr Ala Asn Ile Gln Glu Asn Tyr Pro Arg Gln Pro Pro Ile Trp
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287 Phe Ser Glu Ser Asp Asp Val Pro Val Ile Gly Met Ser Leu Gln Arg
288 65                      70                      75                      80
290 Leu Thr Glu Thr Glu Glu Ser Thr Asn Ile Leu His Gln Val His Arg
291                      85                      90                      95
293 Leu Val Ser Asp Leu Cys Ser Phe Tyr Asn Leu Gln Met Pro Cys Glu
294                      100                      105                      110
296 Leu Pro Gln Ile Ala Pro Pro Val Arg Asp Asp Ile Asp Glu Gly Arg
297                      115                      120                      125
299 Gly Ser Asp Ile Ser Asp Thr Thr Ser Glu Pro Ile Asp Asp Asp Met
300                      130                      135                      140
302 Ala Gly Asp Gly Glu Val Asp Asp Asp Asp Glu Glu Glu Asp Asp
303 145                      150                      155                      160
305 Glu Asp Ala Asp Gly Asp Ile Glu Ile Val Glu Met Ala Glu Glu Asp
306                      165                      170                      175
308 Pro Thr Ser Gln His Asp Val Gly Val Ser Lys Glu Gly Leu Asp Met
309                      180                      185                      190
311 Leu Asp Lys Val Ser Lys Ile Asn Arg Gln Gln His Leu Asp Gly Lys
312                      195                      200                      205
314 Val Gln Gly Ser Ile Thr Ala Thr Asp Arg Leu Met Lys Glu Ile Arg
315                      210                      215                      220
317 Asp Ile His Arg Ser Glu His Phe Lys Asn Gly Ile Tyr Thr Phe Glu
318 225                      230                      235                      240
320 Leu Glu Lys Glu Glu Asn Leu Tyr Gln Trp Trp Ile Lys Leu His Lys
321                      245                      250                      255
323 Val Asp Glu Asp Ser Pro Leu Phe Glu Asp Met Lys Lys Leu Lys Lys
324                      260                      265                      270
326 Asp His Asn Gln Asp His Leu Leu Phe Ser Phe Thr Phe Asn Glu Lys
327                      275                      280                      285
329 Phe Pro Cys Asp Pro Pro Phe Val Arg Val Val Ala Pro His Ile Asn
330                      290                      295                      300
332 Gln Gly Phe Val Leu Gly Gly Ala Ile Cys Met Glu Leu Leu Thr
333 305                      310                      315                      320
335 Lys Gln Gly Trp Ser Ser Ala Tyr Ser Ile Glu Ser Cys Ile Leu Gln
336                      325                      330                      335
338 Ile Ala Ala Thr Leu Val Lys Gly Arg Ala Arg Ile Ser Phe Asp Ala
339                      340                      345                      350
341 Lys His Thr Ser Thr Tyr Ser Met Ala Arg Ala Gln Gln Ser Phe Lys
342                      355                      360                      365
344 Ser Leu Gln Gln Ile His Ala Lys Ser Gly Cys Thr Phe Leu Cys Ser
345                      370                      375                      380
347 Thr Pro Ser Ser His Phe Phe Ala Leu His Leu Val Phe Phe Leu His
348 385                      390                      395                      400
350 Ser Asp Asp Phe Phe Phe Asn Gly Phe Leu Lys Ser Glu Thr Phe Thr
351                      405                      410                      415
353 Phe Phe Lys Leu Ser Phe Arg Gly Tyr Ile Ser Ser Leu Val Leu Tyr
354                      420                      425                      430
356 Ser Phe Ser Arg His Leu His His Pro Phe Phe Thr Arg Phe Leu Ile

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VERIFICATION SUMMARY

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L:17 M:270 C: Current Application Number differs, Replaced Application Number

L:18 M:271 C: Current Filing Date differs, Replaced Current Filing Date